

Vectors of spotted fever in Brazil – a case report in Paraná and the situation of the disease on the country

Vetores da febre maculosa no Brasil – relato de caso no Paraná e a situação da doença no país

Thamy S. Ribeiro^{1*}, Antonio M. Antonucci², Gilberto C. Pavanelli³

Resumo

Febre Maculosa Brasileira (FMB) é uma antroponose causada pela *Rickettsia rickettsii*, altamente patogênico e geneticamente bactérias variável, apresentando vários genótipos virulentos circulantes, com uma grande variação na morbidade e mortalidade da população sensível a esta doença. A fim de identificar as espécies de carrapatos presentes nas capivaras do Parque Estadual do Rio Paraná, 10 espécimes de capivaras (*Hydrochoeris hydrochaeris*) foram coletados em abril de 2012, na planície de inundação do Alto Rio Paraná, entre os Estados de Mato Grosso do Sul e Paraná. Nestas amostras, muitos carrapatos foram recolhidos por catação e levados à Universidade Federal de Uberlândia (UFU) para identificação. Todas as capivaras encontraram-se parasitadas por grande número de indivíduos da espécie *Amblyomma cajennense* e *A. dubitatum*, com os espécimes depositados na Coleção da UFU nos lotes 638 e 639. A presença de carrapatos é relativa, como o *Amblyomma* é o principal vetor da bactéria *R. rickettsii*, a causa de BSF. Com a expansão das áreas urbanas, em que a presença de predadores naturais da capivara é reduzida, além da proibição da caça de capivara nativa no país, houve uma expansão significativa das áreas onde este mamífero é registrado, causando uma profunda mudança nos aspectos eco-epidemiológicos da doença. Este trabalho também pretende contribuir para o aumento da divulgação sobre o BSF, considerando a limitada disponibilidade de informação sobre esta doença no Estado do Paraná.

Abstract

Brazilian Spotted Fever (BSF) is an anthroponosis caused by the *Rickettsia rickettsii*, highly pathogenic and genetically variable bacteria, presenting several virulent circulating genotypes with wide variation in morbidity and mortality of the population sensitive to this disease. In order to identify

the tick species present in capybaras of the State Park of the Paraná River Wetlands, 10 specimens of capybaras (*Hydrochoeris hydrochaeris*) were collected in April 2012, in the Upper Paraná River floodplain, between the States of Mato Grosso do Sul and Paraná. In these specimens, many ticks were collected by picking method and taken to the Federal University of Uberlândia (UFU) for identification. All capybaras found themselves parasitized by large number of individuals of the species *Amblyomma cajennense* and *A. dubitatum*, with the specimens deposited in the Collection of UFU in lots 638 and 639. The presence of ticks is concerning, as the *Amblyomma* is the main vector of the bacterium *R. rickettsii*, the cause of BSF. With the expansion of urban areas, where the presence of natural predators of the capybara is reduced, besides the hunting ban on native capybara in the country, there was a significant expansion of the areas where this mammal is registered, causing a profound change in the ecoepidemiologic characteristics of this disease. This work also intends to contribute on increasing the disclosure about the BSF, considering the limited information availability about this disease in the Paraná State.

Key words: *Amblyomma* sp., BSF, *Rickettsia*,

Introduction

The Spotted Fever, initially called Spotted Fever Rocky Mountain (SFRM), has as etiologic agent the *Rickettsia rickettsii* bacterium (RICKETTS, 1906), which was first identified in the State of Idaho in the United States in the year 1899 (RICKETTS, 1909a,b; HARDEN, 1990). Studies conducted on the 30s concluded that the disease, known

¹PhD Student on Inland Aquatic Environments Ecology Program – Nupélia, State University of Maringá (UEM), Colombo Avenue, 5.790, Zip Code 87020-900, Maringá, Paraná, Brazil; ²Veterinary, PhD on Ichthyoparasitology Laboratory – Nupélia, UEM – and Professor on Veterinary Graduation Course of FAEF, Garça, São Paulo, Brazil; ³ PhD Professor on UEM, Researcher on Limnology, Ichthyology and Aquaculture Research Center (Nupélia). (*thamysantos@yahoo.com.br).

in Brazil as typhus or petechial fever, is transmitted by ticks *Amblyomma cajennense* (PIZA et al., 1932; DIAS et al., 1937; PHILIP et al., 1978).

Currently, the Brazilian Spotted Fever (BSF) is considered a re-emerging zoonosis in Brazil and of great impact to public health due to the difficulty of diagnosis and high mortality in human cases not early treated (GALVÃO et al., 2002; GRECA et al., 2008). The occurrence of the disease in humans has been reported since the '20s in different Brazilian States, being recognized for the first time in Brazil in 1929, in São Paulo; soon after, it was described in Minas Gerais and Rio de Janeiro (DIAS & MARTINS, 1939; GALVÃO, 1988; MELLES et al., 1992; LEMOS et al., 1994; CALIC et al., 1998; LEMOS et al., 1996, 2001; DEL FIOLE et al., 2010).

The microorganisms of the *Rickettsia* genus are representatives of Rickettsiaceae Family and Rickettsiales Order, behaving as Gram negative, pleomorphic, small (0.3 to 0.5 microns by 0.8 to 2.0 microns) and coccobacillus morphology (XU & RAOULT, 1998). It is an obligate intracellular organism, whose main target on vertebrates are endothelial cells, in which the agent is multiplied causing vasculitis (GREENE & BREITSCHWERT, 2006). In arthropod vectors, the *Rickettsia* remains in intestinal cells, salivary glands and ovaries, where they reproduce and cause high levels of mortality in these vectors (RAOULT & ROUX, 1997; RAOULT et al., 2005).

Initially, only the *R. rickettsii* has been described as the cause of spotted fever, but during the last decade, more than 23 species have been validated in Spotted Fever Group (SFG), distributed in every continent except Antarctica, and whose transmission is associated with ticks. In humans, at least 14 species of SFG have been linked to the transmission of spotted fever (*R. aeschlimannii*, *R. africae*, *R. akari*, *R. australis*, *R. conorii*, *R. felis*, *R. helvetica*, *R. honei*, *R. japonica*, *R. marmionii*, *R. mongolotimonae*, *R. parkeri*, *R. sibirica*, *R. slovaca*) (LABRUNA, 2009; PAROLA et al., 2009; CRAGUN et al., 2010; GARCIA-GARCIA et al., 2010). However, *R. rickettsii*

is still considered the main etiological agent of SFG and the most pathogenic for humans, due to the variation in the virulence of circulating genotypes of bacteria (RAOULT & ROUX, 1997; RAOULT et al., 2002; PAROLA et al., 2009).

And with that, the genus *Rickettsia* has recently been divided into four distinct groups: 1) the Spotted Fever Group (SFG); 2) the Typhus Group (TG), which contains the species *R. prowazekii* (causative agent of epidemic typhus transmitted by lice, especially the species *Pediculus humanus humanus*), and *R. typhi* (endemic or murine typhus agent, transmitted by the genus *Xenopsylla* flea); 3) the Transition Group (TG) that contains *R. felis* (associated with the genus *Ctenocephalides* fleas) and *R. akari* (associated with small mites *Allodermmanyssus* gender); 4) and Ancestral Group (AG) formed by the species *R. bellii* and *R. canadensis*, both of unknown pathogenicity to humans and non-human animals (RAOULT & ROUX, 1997; EREMEEVA et al., 2000; GILLESPIE et al., 2007).

The study of the ecology of bacteria of the genus *Rickettsia* is very important, particularly in the evaluation of different tick populations and the role of these microorganisms on the propagation of spotted fever, considering that, once infected by a tick species of *Rickettsia*, the tick becomes refractory to infection by a second species of *Rickettsia* (BURGDORFER et al., 1981).

The better accepted taxonomic classification of ticks inserts them on the Phylum Arthropoda, Class Arachnida, Subclass Acari. The main families of public health interest are Ixodidae, Argasidae and Nuttalliella, however the latter is restricted to the African continent while the others are cosmopolitan (BARROS-BATTESTI et al., 2006). All species require blooded vertebrates as a food source and have significant degree of specificity, mostly. However, ticks can use alternative hosts, as the man, and some factors may favor the transmission of pathogens, such as smaller relation host/parasite, lower degree of specificity of ticks, and long periods of fasting, what characterizes the Ixodidae Family as the most pathogenic (BARROS-BATTESTI et al., 2006; MONTEIRO, 2014).

The most important vectors of the spotted fever present: adaptations to different hosts, which allows a better placement of pathogens between species; longevity of the stages in the environment, providing time for multiplication of pathogens; transovarian transmission, allowing the viability of pathogens in successive generations while acting as efficient reservoirs (HARWOOD & JAMES, 1979). Because of these characteristics, the ticks of the genus *Amblyomma* is of great importance on the transmission of this disease, besides its wide distribution in the Americas (MASSARD & FONSECA, 2004).

Given the importance of ticks in the transmission of FMB, this study aimed to raise qualitatively both the species level as the development stage of ticks that may be infesting the capybaras (*Hydrochoeris hydrochaeris*) in the upper Paraná River floodplain, near the municipality of Porto Rico, PR.

Material e methods

The Paraná River floodplain is the last not dammed stretch of this river in Brazil (22 ° 40'-22 ° 45 'S and 53 ° 15'-53 ° 25' W).

Capybaras were killed with shotgun near the Bay River in April 2012, with the authorization of the environmental agency responsible (ICMBIO/SISBIO, environmental license No. 28858-1, of 11/08/2011). In these specimens, several individuals of ticks, adults and nymphs, were collected by picking method and taken to the Federal University of Uberlândia (UFU) for identification.

Results e Discussion

In Brazil the tick *A.cajennense* is the main vector of BSF, found in abundance in the South Central region and with few reports in the North-Northeast region of the country (Horta et al., 2004; Sangioni et al., 2005). The tick *A.cajennense* is trioxeno, i.e., requires three hosts to complete its life cycle, and horses (*Equus caballus*), tapirs (*Tapirus terrestris*) and capybaras (*H. hydrochaeris*) are the main hosts of this vector. However, when the tick population is increased, it can feed a wide variety of vertebrate hosts.

Among these, the domestic dog deserves attention and is often found infested with *A.cajennense* in different areas of Brazil (LABRUNA & PEREIRA, 2001), facilitating the spread of disease in humans who have contact with dogs (MONTEIRO, 2014).

The development of *A. cajennense* occurs over 1 year with three parasitic stages. The hexapod nymphs (larvae) occur between March and July and survive up to 6 months without food. The octopuses nymphs occur between July and November, and adults, from November to March and can survive up to 1 and 2 years, respectively, without feeding.

The species *A. aureolatum*, popularly known as 'yellow-tick', is also considered an important vector and a reservoir of the BSF, found in Atlantic forest areas of South and Southeast regions, where high humidity conditions and mild temperatures prevail throughout the year (PINTER et al., 2004; MORAES-FILHO et al., 2009). Canids, including domestic dogs, are the main hosts for adults of this tick species and, on rural environments near remnants of tropical forest, *A. aureolatum* may infest domestic dogs, representing a potential risk to human transmission (Tomassone et al., 2010).

The species *A. cooperi* (*dubitatum*) is also presented as a possible transmitter of BSF, but further studies are needed to prove the ecological role of this species (LEMOS et al., 1996; LABRUNA et al., 2004).

The tick bite, in any of its stages (larva or adult), is the main form of transmission of *Rickettsia* sp. (PAROLA et al., 2005). To transmit the disease, the ticks must be attached to the skin, feeding for a period of 4 to 10 hours, the time required for reactivation of the bacteria to its virulent state (CHEN & SEXTON, 2008; DEL FIOLE et al., 2010). By biting, during feeding, the tick transmits the organism through its salivary glands. It is important to note that the bites of larvae and nymphs, as they are less painful, are the ones most likely to transmit the bacterium, because the host does not notice the bite and allows the transmission to occur. Another form of infection occurs by crushing the tick when it is removed, releasing the infectious forms (CHEN & SEXTON, 2008).

Infected ticks contain a large amount of rickettsiae in their hemolymph, and the transmission of the agent may also occur during the removal of the arthropod - the excessive pressure may cause the tick to rupture, increasing the risk of contamination (RAOULT and PAROLA, 2007). In several reports of infection by *R. rickettsii* in humans, manual removal of ticks was the only known risk factor associated with the development of the disease (SHEPARD & TOPPING, 1946; SEXTON & BURGDORFER, 1975).

The present study found adults and larvae of *A. cajennense* and *A. dubitatum*, and the specimens were deposited in the Ticks Collection of the Federal University of Uberlândia (lots 638 and 639). Ticks are responsible for maintaining *R. rickettsii* in nature, acquiring this bacterium during biting an infected host or by transovarian (transmission of bacteria between successive generations) and transtadial transmission (agent survival in all stages of life) (STANCZAK et al., 2009). These features allow the tick remains infected throughout their life and also for many generations after primary infection (BRASIL, 2005).

However, this mechanism only is not sufficient to maintain the bacteria on an active performance over time, in view of the deleterious effect that it causes on ticks (MCDADE & NEWHOUSE, 1986). It is believed that some vertebrates has a fundamental role in the maintenance of the pathogen in nature while maintaining the bacterium for days or weeks and amplifying *R. rickettsii* infection in non-infected ticks before (BURGDORFER, 1988).

The BSF, due to its public health importance, was included in the national list of reportable diseases and these notifications, which became part of the National Notifiable Diseases System (SINAN), are facilitating the implementation of trend analysis and promotion practices that seek to reduce morbidity and mortality (BRASIL, 2009).

BARROS e SILVA et al. (2014) observed that 9644 cases of BSF were reported from 2007 to 2012 all over the country, with a probability of infection in São Paulo (44.14%), Santa Catarina (24.52%), Minas Gerais (8.7%), Rio de Janeiro (6.5%),

Espírito Santo (2.6%), Paraná (1.63%), Rio Grande do Sul (0.7%), Bahia (0.54%), Goiás (0.4%) and Ceará (0.27%). The age group most affected by BSF fever was 35-49 years old (26.83%), the average age was 42 years and the male was the most prevalent group (68.4%). These same authors observed that the disease has small fluctuations in the periods January to June, followed by an increase in the peak occurs from July to December; during this period the *A. cajennense*, primary vector of disease in Brazil, is in its larval stage, the form predominantly known as parasitic in humans (LABRUNA et al., 2002).

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